Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/14 06:17:45

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6008671.sorted.bam -c -nw 400 -hm 3
```

1.2. Alignment

Command line:	/home/luna/Desktop/Software/bwa/bwa mem -t 16 -k 30 -R @RG\tID:Singlecell2022\tLB:Library\tPL:ILLUMINA\tSM:sample_SRR6008671 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6008671.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 14 06:17:44 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6008671.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	4,554,317
Mapped reads	3,801,864 / 83.48%
Unmapped reads	752,453 / 16.52%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	38,293 / 0.84%
Read min/max/mean length	30 / 76 / 76.29
Duplicated reads (estimated)	449,291 / 9.87%
Duplication rate	8.98%
Clipped reads	1,853,581 / 40.7%

2.2. ACGT Content

Number/percentage of A's	69,792,484 / 28.04%
Number/percentage of C's	46,166,297 / 18.55%
Number/percentage of T's	78,925,183 / 31.71%
Number/percentage of G's	53,923,340 / 21.67%
Number/percentage of N's	73,522 / 0.03%
GC Percentage	40.22%

2.3. Coverage

Mean	0.0804

Standard Deviation	0.7452

2.4. Mapping Quality

Mean Mapping Quality	43.4

2.5. Mismatches and indels

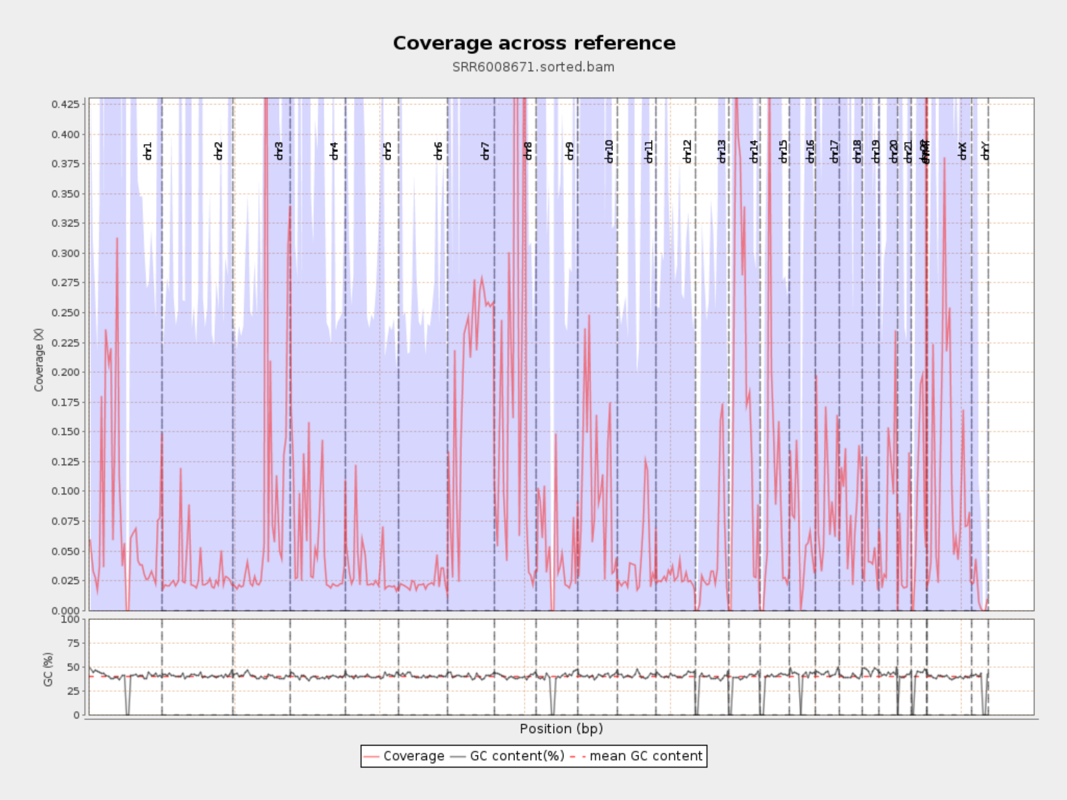
General error rate	0.87%
Mismatches	2,132,828
Insertions	22,418
Mapped reads with at least one insertion	0.58%
Deletions	73,659
Mapped reads with at least one deletion	1.91%
Homopolymer indels	47.28%

2.6. Chromosome stats

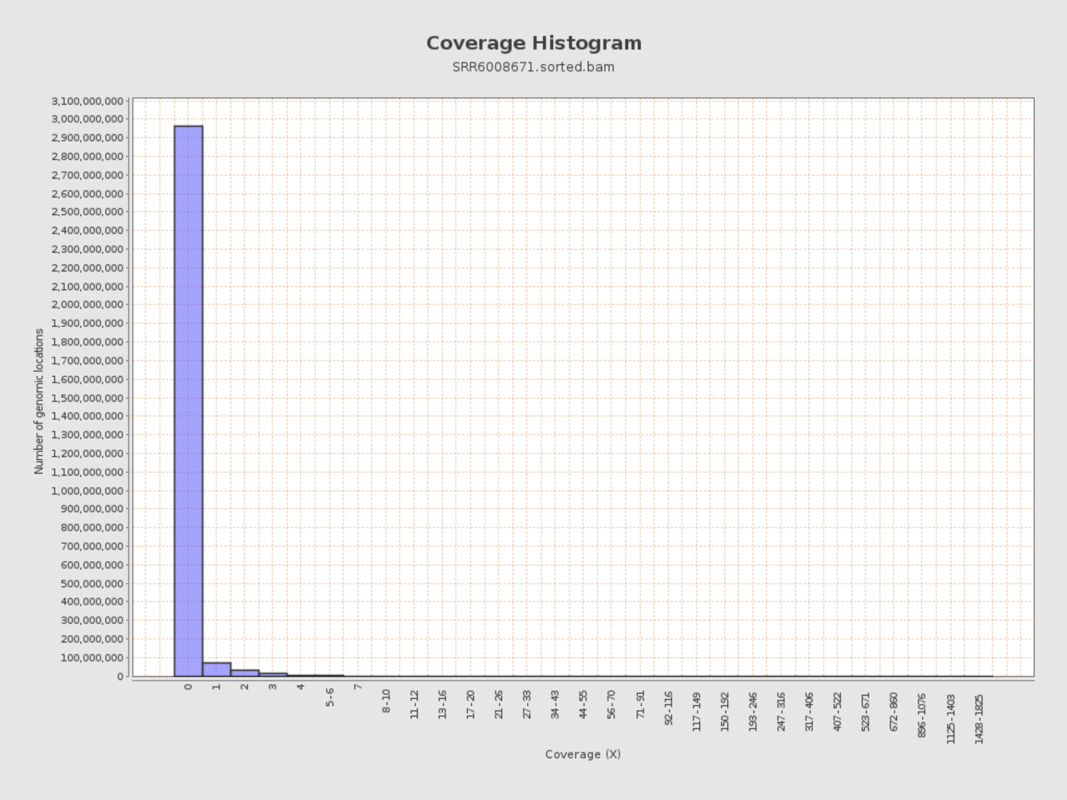
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	18974527	0.0761	0.6232
chr2	243199373	7480050	0.0308	0.6423
chr3	198022430	18284256	0.0923	0.5878
chr4	191154276	10894429	0.057	0.4668
chr5	180915260	6269452	0.0347	0.3085
chr6	171115067	4011025	0.0234	0.2719
chr7	159138663	32257553	0.2027	0.995

chr8	146364022	27816078	0.19	0.8295
chr9	141213431	7076441	0.0501	0.7452
chr10	135534747	14738041	0.1087	1.575
chr11	135006516	5570626	0.0413	0.616
chr12	133851895	3719918	0.0278	0.2847
chr13	115169878	5096943	0.0443	0.3438
chr14	107349540	20367848	0.1897	0.7583
chr15	102531392	10231110	0.0998	0.5311
chr16	90354753	5818210	0.0644	0.6533
chr17	81195210	8495960	0.1046	0.5476
chr18	78077248	6918836	0.0886	1.9382
chr19	59128983	2915243	0.0493	0.5377
chr20	63025520	6191772	0.0982	0.5127
chr21	48129895	2490103	0.0517	0.438
chr22	51304566	4747729	0.0925	0.4954
chrMT	16571	107098	6.463	4.929
chrX	155270560	17762235	0.1144	0.8576
chrY	59373566	767399	0.0129	0.35

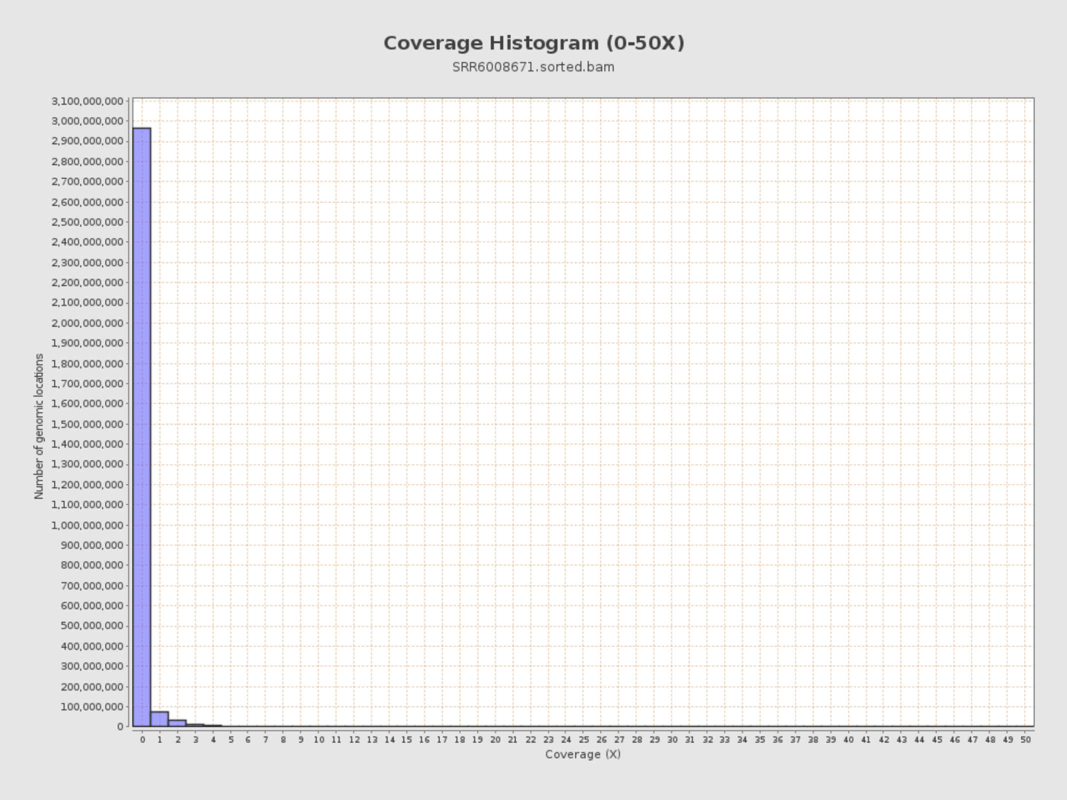
3. Results : Coverage across reference



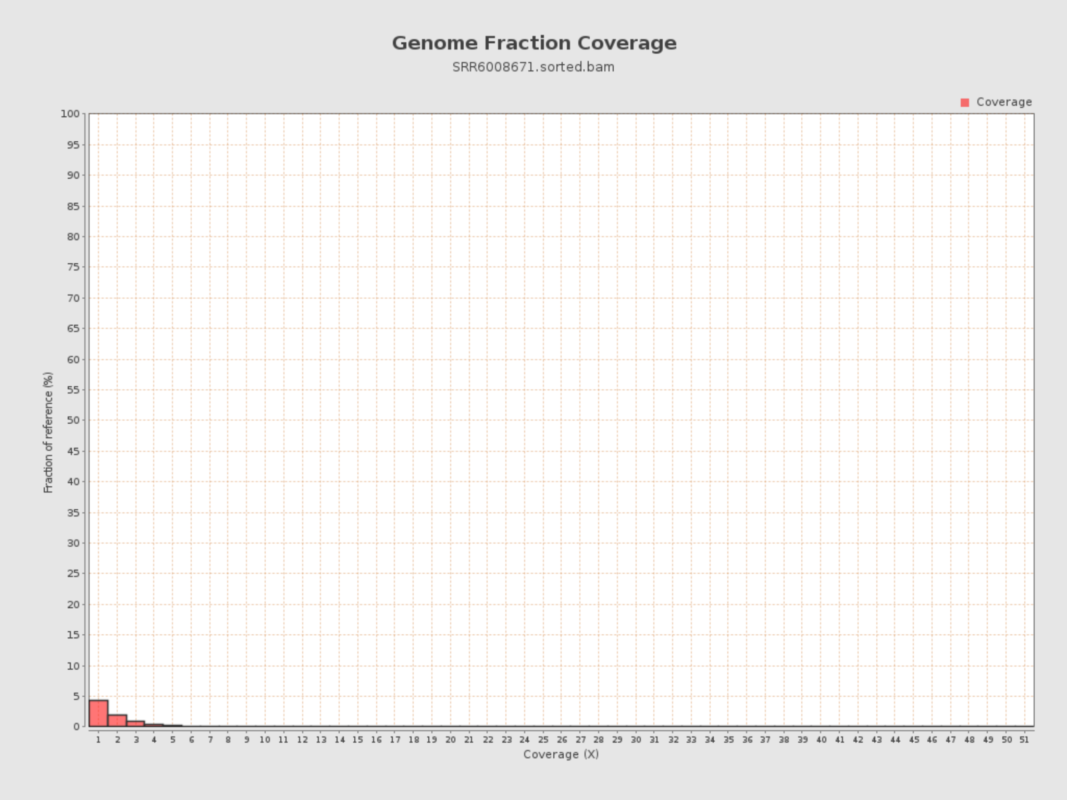
4. Results : Coverage Histogram



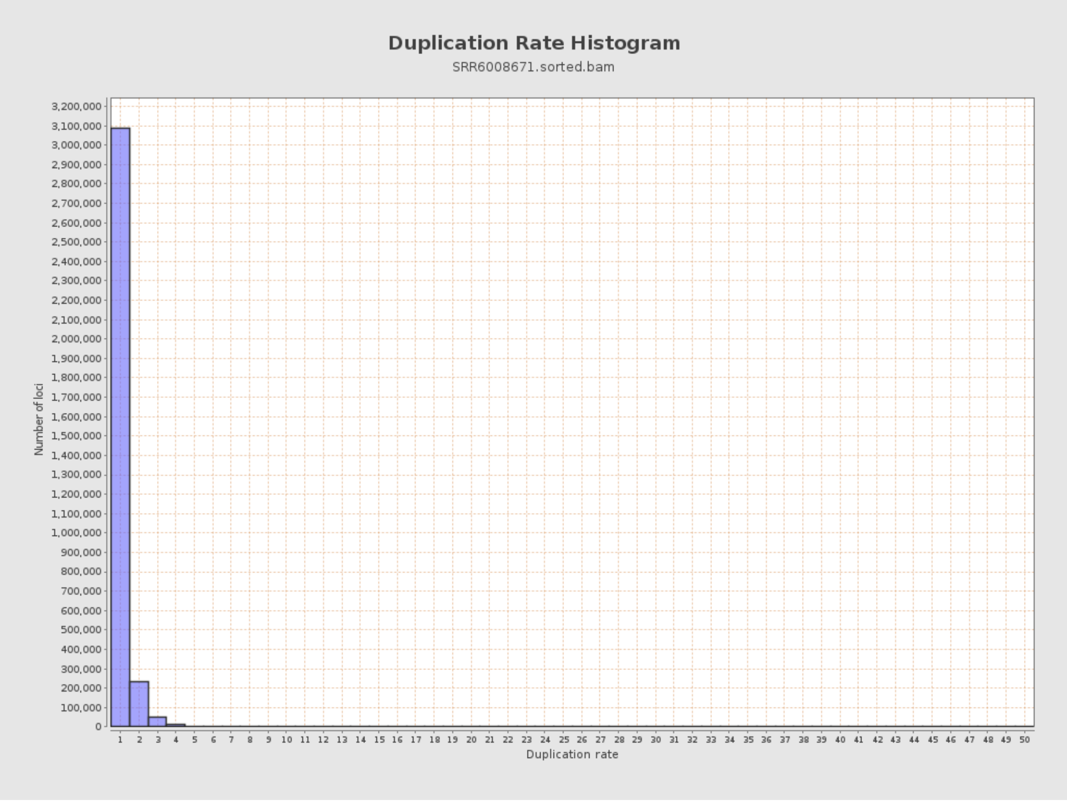
5. Results : Coverage Histogram (0-50X)



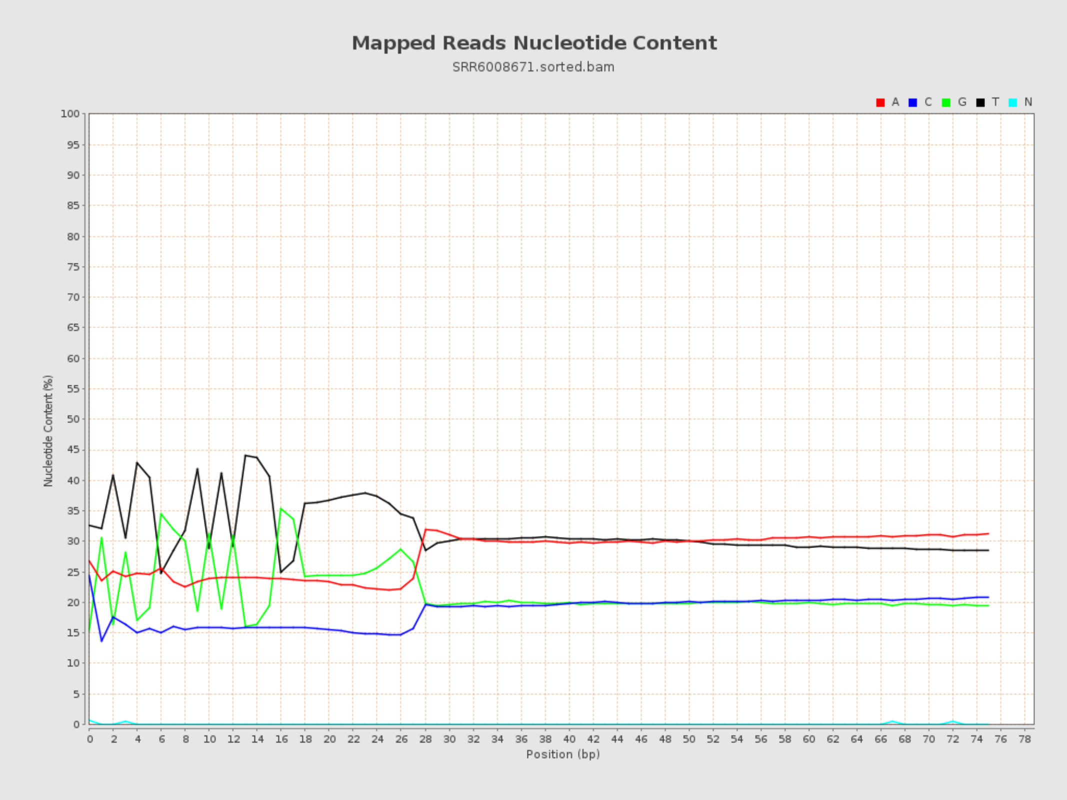
6. Results : Genome Fraction Coverage



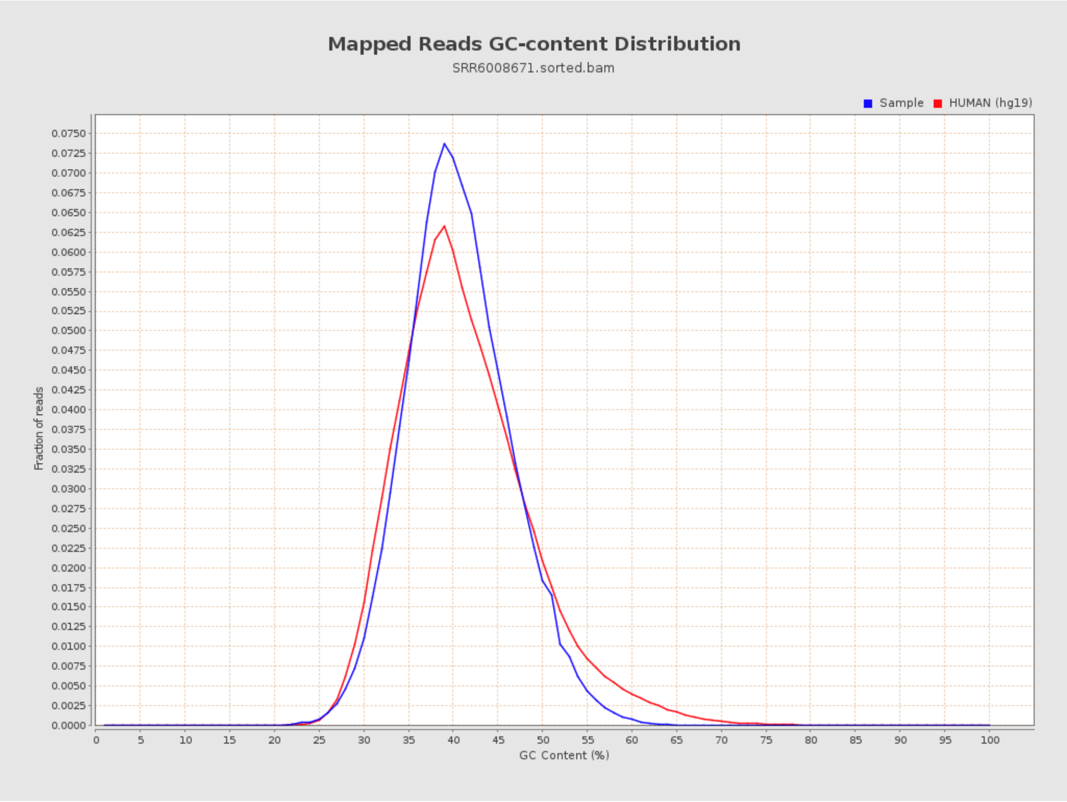
7. Results : Duplication Rate Histogram



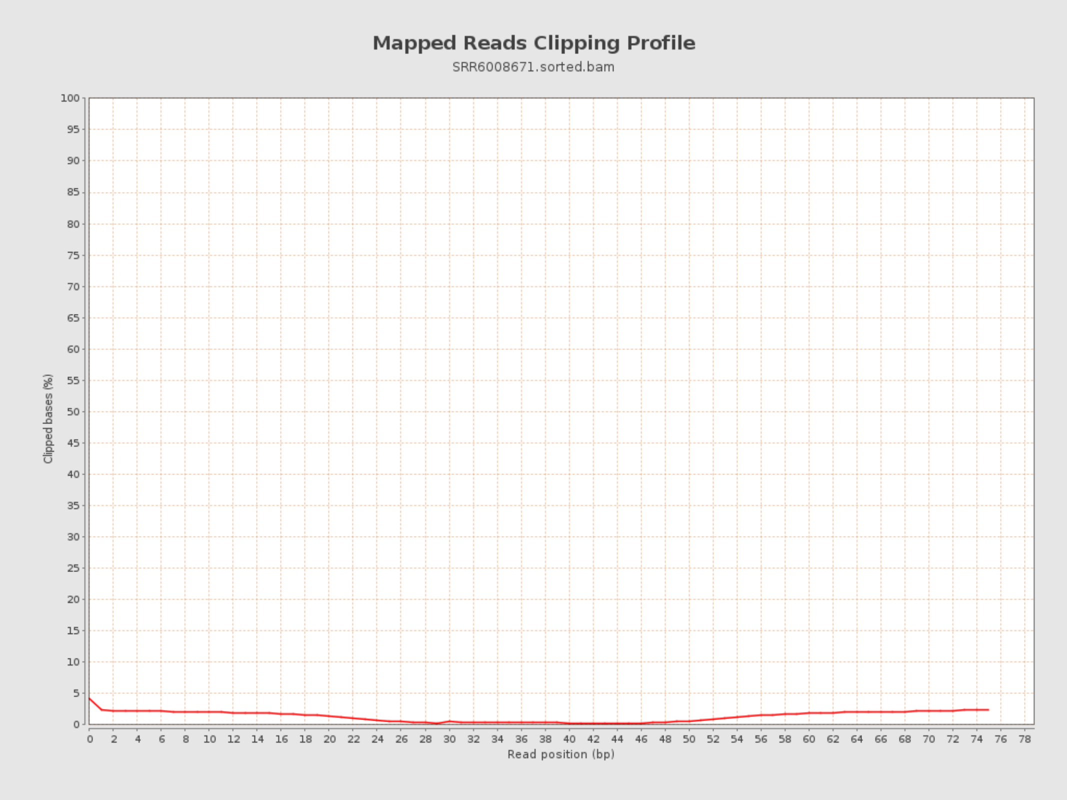
8. Results : Mapped Reads Nucleotide Content



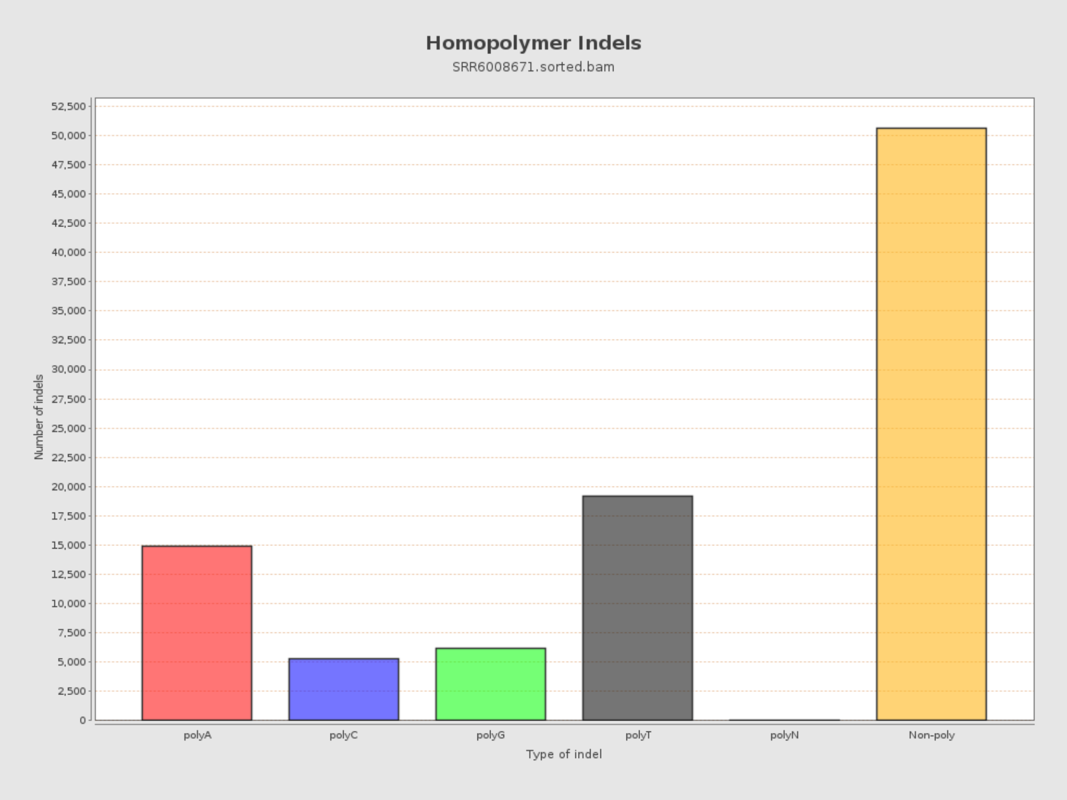
9. Results : Mapped Reads GC-content Distribution



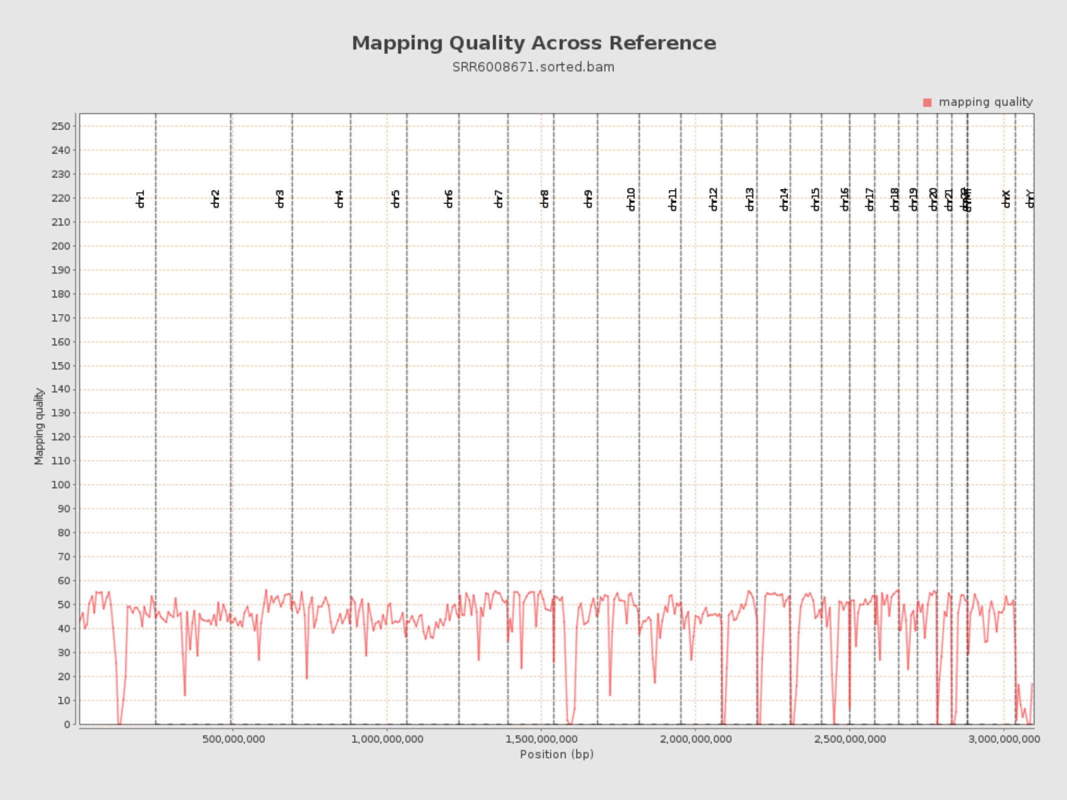
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram